

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Sutcliffe, J. Gregor  
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(ii) TITLE OF INVENTION: Hypothalamus-Specific Polypeptides

(iii) NUMBER OF SEQUENCES: 15

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Olson & Hierl, Ltd.  
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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: Not yet Known (Division of 09/230,896  
filed 02-FEB-1999)  
(B) FILING DATE: Herewith  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/023,220  
(B) FILING DATE: 02-AUG-1996  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Talivaldis Cepuritis  
(B) REGISTRATION NUMBER: 20,818  
(C) REFERENCE/DOCKET NUMBER: TSRI 548.1 DIV.1

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 130 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Asn	Leu	Pro	Ser	Thr	Lys	Val	Pro	Trp	Ala	Ala	Val	Thr	Leu	Leu
1				5					10					15	
Leu	Leu	Leu	Leu	Leu	Pro	Pro	Ala	Leu	Leu	Ser	Leu	Gly	Val	Asp	Ala
			20					25					30		
Gln	Pro	Leu	Pro	Asp	Cys	Cys	Arg	Gln	Lys	Thr	Cys	Ser	Cys	Arg	Leu
		35					40					45			
Tyr	Glu	Leu	Leu	His	Gly	Ala	Gly	Asn	His	Ala	Ala	Gly	Ile	Leu	Thr
	50					55						60			
Leu	Gly	Lys	Arg	Arg	Pro	Gly	Pro	Pro	Gly	Leu	Gln	Gly	Arg	Leu	Gln
65					70					75					80
Arg	Leu	Leu	Gln	Ala	Asn	Gly	Asn	His	Ala	Ala	Gly	Ile	Leu	Thr	Met
				85					90					95	
Gly	Arg	Arg	Ala	Gly	Ala	Glu	Leu	Glu	Pro	Tyr	Pro	Cys	Pro	Gly	Arg
			100					105					110		
Arg	Cys	Pro	Thr	Ala	Thr	Ala	Thr	Ala	Leu	Ala	Pro	Arg	Gly	Gly	Ser
		115					120					125			
Arg	Val														
	130														

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 130 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Asn	Phe	Pro	Ser	Thr	Lys	Val	Pro	Trp	Ala	Ala	Val	Thr	Leu	Leu
1				5					10					15	
Leu	Leu	Leu	Leu	Leu	Pro	Pro	Ala	Leu	Leu	Ser	Leu	Gly	Val	Asp	Ala
			20					25					30		

Gln Pro Leu Pro Asp Cys Cys Arg Gln Lys Thr Cys Ser Cys Arg Leu  
35 40 45  
Tyr Glu Leu Leu His Gly Ala Gly Asn His Ala Ala Gly Ile Leu Thr  
50 55 60  
Leu Gly Lys Arg Arg Pro Gly Pro Pro Gly Leu Gln Gly Arg Leu Gln  
65 70 75 80  
Arg Leu Leu Gln Ala Asn Gly Asn His Ala Ala Gly Ile Leu Thr Met  
85 90 95  
Gly Arg Arg Ala Gly Ala Glu Leu Glu Pro His Pro Cys Ser Gly Arg  
100 105 110  
Gly Cys Pro Thr Val Thr Thr Thr Ala Leu Ala Pro Arg Gly Gly Ser  
115 120 125  
Gly Val  
130

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 569 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TAAGACGACG GCCTCAGACT CCTTGGGTAT TTGGACCACT GCACCGAAGA TACCATCTCT	60
CCGGATTACC TCTCCCTGAG CTCCAGACAC CATGAACCTT CCTTCTACAA AGGTTCCTTG	120
GGCCGCCGTG ACGCTGCTGC TGCTGCTACT GCTGCCGCCG GCGCTGCTGT CGCTTGGGGT	180
GGACGCGCAG CCTCTGCCCC ACTGCTGTCG CCAGAAGACG TGTTCCCTGCC GGCTCTACGA	240
ACTGTTGCAC GGAGCTGGCA ACCACGCCGC GGGCATCCTC ACTCTGGGAA AGCGGCGACC	300
TGGACCCCCA GGCCTCCAAG GACGGCTGCA GCGCCTCCTT CAGGCCAACG GTAACCACGC	360
AGCTGGCATC CTGACCATGG GCCGCCGCGC AGGCGCAGAG CTAGAGCCAT ATCCCTGCCC	420
TGGTCGCCGC TGTCCGACTG CAACCGCCAC CGCTTTAGCG CCCCAGGGGCG GATCCAGAGT	480
CTGAACCCGT CTTCTATCCC TGTCCTAGTC CTAACCTTCC CCTCTCCTCG CCAGTCCCTA	540
GGCAATAAAG ACGTTTCTCT GTTGGTGTG	569

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 582 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TAAGACGACG GCCTCAGACT TCTTGGGTAT TTGGACCACT GCACTGAAGA GATCATCTCT	60
CCAGATTACT TTCCCCTGAG CTCCAGGCAC CATGAAC TTT CTTCTACAA AGGTTCCCTG	120
GGCCGCCGTG ACGCTGCTGC TGCTGCTACT GCTGCCACCG GCGCTGCTGT CGCTTGGGGT	180
GGACGCACAG CCTCTGCCCC ACTGCTGTCTG CCAGAAGACG TGTTCCTGCC GTCTCTACGA	240
ACTGTTGCAC GGAGCTGGCA ACCACGCTGC GGGTATCCTG ACTCTGGGAA AGCGGCGGCC	300
TGGACCTCCA GGCCTCCAGG GACGGCTGCA GCGCCTCCTT CAGGCCAACG GTAACCACGC	360
AGCTGGCATC CTGACCATGG GCCGCCGCGC AGGCGCAGAG CTAGAGCCAC ATCCCTGCTC	420
TGGTCGCGGC TGTCCGACCG TAACTATCAC CGCTTTAGCA CCCCGGGGAG GTCCGGAGT	480
TTGAACCCAT CTTCTATCCT TGTCTGATC CAACTTCCC CCTCTGCTCG CCGCTGTCAG	540
TCTCTTGGTA AATGGCAATA AAGACGTTTC TCTGTTGGTG TG	582

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1458 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCTAGGAGAC ATTGCGGCGG CGGTGGCGGC GTTGGCAGCA GCTGCAGACA TGCTGCTGCT	60
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CAAGAAACAG ACGGAGGACA TCAGCAGTGT CTATGAGATC CGGGAGAAGC TGGGCTCGGG	120
TGCCTTCTCT GAGGTGATGC TGGCCCAGGA AAGGGGCTCT GCTCATCTTG TGGCCCTCAA	180
GTGCATTCCC AAGAAAGCAC TTCGGGGCAA GGAGGCCCTG GTGGAGAATG AGATCGCAGT	240
ACTCCGCAGG ATTAGCCACC CCAACATTGT GGCTCTGGAG GACGTCCACG AGAGCCCTTC	300
CCATCTCTAC TTGGCCATGG AGCTGGTAAC AGGTGGTGAA CTGTTTGACC GAATCATGGA	360
GCGGGGCTCC TACACAGAGA AGGATGCGAG CCACCTTGTA GGGCAGGTCC TTGGTGCTGT	420
CTCTACCTT CATAGCCTGG GCATCGTGCA CCGGGACCTC AAGCCTGAAA ACCTCCTCTA	480
TGCCACACCT TTTGAGGACT CCAAGATCAT GGTCTCTGAC TTTGGCCTGT CCAAATTC	540
AGCTGGCAAC ATGCTAGGCA CAGCCTGTGG GACCCAGGA TATGTGGCCC CAGAGCTCCT	600
GGAGCAGAAA CCCTACGGGA AGGCCGTAGA TGTGTGGGCC CTGGGTGTCA TCTCTACAT	660
CCTGCTGTGT GGGTACCCCC CTTTCTATGA TGAGAGCGAT CCTGAACTCT TCAGCCAGAT	720
TCTGAGGGCC AGCTACGAGT TTGACTCTCC CTTTGGGAT GACATCTCAG AATCAGCCAA	780
AGACTTCATT CGGCACCTTC TGGAACGTGA TCCCCAGAAG AGGTTACCT GCCAACAGGC	840
CTTACAGCAT CTCTGGATCT CTGGGGATGC AGCCTTGAC AGGGACATCC TAGGTTCTGT	900
CAGTGAGCAG ATCCAGAAGA ATTTTGCCAG GACCCACTGG AAGCGTGCAT TCAATGCCAC	960
ATCATTCCTA CGTCACATCC GTAAGCTGGG ACAGAGCCCA GAGGGTGAGG AGGCCTCCAG	1020
GCAGGGTATG ACCCGTCACA GCCACCCAGG CCTTGGGACT AGCCAGTCTC CCAAGTGGTG	1080
ACAACCAGGT GGATGCCAAG GAAGGCCAAG TGGACTGACT CCTAGCTTTT CTTTCCTCCA	1140
GCCCTTTTGA TCTCCTTCCC TGATCCTTGT CCCCCGACT GGCCTCTGTT GGAAAGTCCA	1200
AGACCGTGGG TGTGATGCAT GGCCTGGGG TATGGGGCTT CCAAGTATG TCCCCAGCCT	1260
CTGTCCTTTG TTGCTGCCAC CCTCTATGGA AACTGAGGAG GTATTCAAAA ATGGATTTGG	1320
GGGCCATCCT TCCTGCACCT TGCACGCACA TATGCATTGC GTGGCTGTTC TGTGCTTTGC	1380
TGACTGTGGG TGGTCCTGCT TGTGTTGTAG CCCTTTAGTT CCTCCTCTTT CCAACCAATA	1440
AAGACAAACA GAACAATG	1458

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 103 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

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Leu Gly Val Asp Ala Gln Pro Leu Pro Asp Cys Cys Arg Gln Lys Thr
1           5           10           15

Cys Ser Cys Arg Leu Tyr Glu Leu Leu His Gly Ala Gly Asn His Ala
          20           25           30

Ala Gly Ile Leu Thr Leu Gly Lys Arg Arg Pro Gly Pro Pro Gly Leu
          35           40           45

Gln Gly Arg Leu Gln Arg Leu Leu Gln Ala Asn Gly Asn His Ala Ala
          50           55           60

Gly Ile Leu Thr Met Gly Arg Arg Ala Gly Ala Glu Leu Glu Pro Tyr
65           70           75           80

Pro Cys Pro Gly Arg Arg Cys Pro Thr Ala Thr Ala Thr Ala Leu Ala
          85           90           95

Pro Arg Gly Gly Ser Arg Val
          100

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(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 39 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

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Leu Gly Val Asp Ala Gln Pro Leu Pro Asp Cys Cys Arg Gln Lys Thr
1           5           10           15

Cys Ser Cys Arg Leu Tyr Glu Leu Leu His Gly Ala Gly Asn His Ala
          20           25           30

Ala Gly Ile Leu Thr Leu Gly
          35

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(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 38 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:

(I) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Leu	Gly	Val	Asp	Ala	Gln	Pro	Leu	Pro	Asp	Cys	Cys	Arg	Gln	Lys	Thr
1				5					10					15	
Cys	Ser	Cys	Arg	Leu	Tyr	Glu	Leu	Leu	His	Gly	Ala	Gly	Asn	His	Ala
			20					25					30		
Ala	Gly	Ile	Leu	Thr	Leu										
			35												

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Pro	Gly	Pro	Pro	Gly	Leu	Gln	Gly	Arg	Leu	Gln	Arg	Leu	Leu	Gln	Ala
1				5				10						15	
Asn	Gly	Asn	His	Ala	Ala	Gly	Ile	Leu	Thr	Met	Gly				
			20					25							

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Pro Gly Pro Pro Gly Leu Gln Gly Arg Leu Gln Arg Leu Leu Gln Ala  
1 5 10 15

Asn Gly Asn His Ala Ala Gly Ile Leu Thr Met  
20 25

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Arg Leu Tyr Glu Leu Leu His Gly Ala Gly Asn His Ala Ala Gly Ile  
1 5 10 15

Leu Thr Leu Gly  
20

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Arg Leu Gln Arg Leu Leu Gln Ala Asn Gly Asn His Ala Ala Gly Ile  
1 5 10 15

Leu Thr Met Gly  
20

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 9 amino acids



(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Gly Asn His Ala Ala Gly Ile Leu Thr  
1 5

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 393 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ATGAACCTTC CTTCTACAAA GGTTCCCTGG GCCGCCGTGA CGCTGCTGCT GCTGCTACTG	60
CTGCCGCCGG CGCTGCTGTC GCTTGGGGTG GACGCGCAGC CTCTGCCCCG CTGCTGTCGC	120
CAGAAGACGT GTTCCTGCCG TCTCTACGAA CTGTTGCACG GAGCTGGCAA CCACGCCGCG	180
GGCATCCTCA CTCTGGGAAA GCGGCGACCT GGACCCCCAG GCCTCCAAGG ACGGCTGCAG	240
CGCCTCCTTC AGGCCAACGG TAACCACGCA GCTGGCATCC TGACCATGGG CCGCCGCGCA	300
GGCGCAGAGC TAGAGCCATA TCCCTGCCCT GGTCGCCGCT GTCCGACTGC AACCGCCACC	360
GCTTTAGCGC CCCGGGGCGG ATCCAGAGTC TGA	393

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 393 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ATGAACTTTC CTTCTACAAA GGTTCCTGG GCCGCCGTGA CGCTGCTGCT GCTGCTACTG	60
CTGCCGCCGG CGCTGCTGTC GCTTGGGGTG GACGCACAGC CTCTGCCCCG CTGCTGTCGC	120
CAGAAGACGT GTTCCTGCCG TCTCTACGAA CTGTTGCACG GAGCTGGCAA CCACGCTGCG	180
GGTATCCTGA CTCTGGGAAA GCGGCGGCCT GGACCTCCAG GCCTCCAGGG ACGGCTGCAG	240
CGCCTCCTTC AGGCCAACGG TAACCACGCA GCTGGCATCC TGACCATGGG CCGCCGCGCA	300
GGCGCAGAGC TAGAGCCACA TCCCTGCTCT GGTCGCGGCT GTCCGACCGT AACTACCACC	360
GCTTTAGCAC CCCGGGGAGG GTCCGGAGTC TGA	393